



SEQUENCE LISTING

<110> Cohen, Stanley N.
Li, Limin

<120> MAMMALIAN TUMOR SUSCEPTIBILITY GENES AND THEIR USES

<130> 70017.27USC2

<140> US 10/697,720
<141> 2003-10-29

<150> US 09/804,690
<151> 2001-03-12

<150> US 09/146,187
<151> 1998-09-01

<150> US 08/977,818
<151> 1997-11-25

<150> US 08/670,274
<151> 1996-06-13

<150> US 08/585,758
<151> 1996-01-16

<150> US 60/006,856
<151> 1995-11-16

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<170> PatentIn version 3.3

<210> 1
<211> 1448
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<220>
<223> TSG101 nucleotide

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<222> (61)..(1203)

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atg atg tcc aag tac aaa tat aga gat cta acc gtc cgt caa act gtc 108
Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val
1 5 10 15

aat gtc atc gct atg tac aaa gat ctc aaa cct gta ttg gat tca tat 156
Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
20 25 30

gtt ttt aat gat ggc agt tcc agg gag ctg gtg aac ctc act ggt aca 204
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr

35	40	45	
atc cca gtg cgt tat cga ggt aat ata tat aat att cca ata tgc ctg Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu	50	55	252
		60	
tgg ctg ctg gac aca tac cca tat aac ccc cct atc tgt ttt gtt aag Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys	65	70	300
		75	
		80	
cct act agt tca atg act att aaa aca gga aag cat gtg gat gca aat Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn	85	90	348
		95	
ggg aaa atc tac cta cct tat cta cat gac tgg aaa cat cca cgg tca Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser	100	105	396
		110	
gag ttg ctg gag ctt att caa atc atg att gtg ata ttt gga gag gag Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu	115	120	444
		125	
cct cca gtg ttc tcc cgg cct act gtt tct gca tcc tac cca cca tac Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr	130	135	492
		140	
aca gca aca ggg cca cca aat acc tcc tac atg cca ggc atg cca agt Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser	145	150	540
		155	
		160	
gga atc tct gca tat cca tct gga tac cct ccc aac ccc agt ggt tat Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr	165	170	588
		175	
cct ggc tgt cct tac cca cct gct ggc cca tac cct gcc aca aca agc Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser	180	185	636
		190	
tca cag tac cct tcc cag cct gtg acc act gtt ggt ccc agc aga Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg	195	200	684
		205	
gat ggc aca atc agt gag gac act atc cgt gca tct ctc atc tca gca Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala	210	215	732
		220	
gtc agt gac aaa ctg aga tgg cgg atg aag gag gaa atg gat ggt gcc Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala	225	230	780
		235	
		240	
cag gca gag ctt aat gcc ttg aaa cga aca gag gaa gat ctg aaa aaa Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys	245	250	828
		255	
ggc cac cag aaa ctg gaa gag atg gtc acc cgc tta gat caa gaa gta Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val	260	265	876
		270	
gct gaa gtt gat aaa aac ata gaa ctt ttg aaa aag aag gat gaa gaa Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu	294		924

275

280

285

ct a agt tct gct ctg gag aaa atg gaa aat caa tct gaa aat aat gat Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp 290 295 300	972
att gat gaa gtt atc att ccc aca gcc cca ctg tat aaa cag att cta Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu 305 310 315 320	1020
aat ctg tat gca gag gaa aat gct att gaa gac act atc ttt tac ctt Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu 325 330 335	1068
gga gaa gct ttg cgg cgg gga gtc ata gac ctg gat gtg ttc ctg aaa Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys 340 345 350	1116
cac gtc cgc ctc ctg tcc cgt aaa cag ttc cag cta agg gca cta atg His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met 355 360 365	1164
caa aag gca agg aag act gcg ggc ctt agt gac ctc tac tgacatgtgc Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr 370 375 380	1213
tgtcagctgg agaccgacct ctccgtaaag cattctttc ttcttcttt tctcatcagt	1273
agaacccaca ataagttatt gcagttatc attcaagtgt taaatatttt gaatcaataa	1333
tatattttct gttcccttg ggtaaaaact ggctttatt aatgcacttt ctaccctctg	1393
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Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr 20 25 30

Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr 35 40 45

Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu 50 55 60

Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
65 70 75 80

Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
85 90 95

Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser
100 105 110

Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu
115 120 125

Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr
130 135 140

Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser
145 150 155 160

Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr
165 170 175

Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser
180 185 190

Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg
195 200 205

Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala
210 215 220

Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala
225 230 235 240

Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys
245 250 255

Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
260 265 270

Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
275 280 285

Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
290 295 300

Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
305 310 315 320

Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
325 330 335

Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
340 345 350

His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
355 360 365

Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
370 375 380

<210> 3
<211> 1494
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<213> Artificial Sequence

<220>
<223> Primer

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atggtgtcca agtacaataa cagagaccta actgtacgtg aaactgtcaa ttttattact 180
ctatacaaag atctcaaacc tttttggat tcatatgttt ttaacgatgg cagttccagg 240
gaactaatga acctcaactgg aacaatccct gtgccttata gaggttaatac atacaatatt 300
ccaatatgcc tatggctact ggacacatac ccatataatc cccctatctg ttttgttaag 360
cctacttagtt caatgactat taaaacagga aagcatgttg atgcaaatgg gaagatataat 420
cttccttatac tacatgaatg gaaacacccca cagtcagact ttggggct tattcaggtc 480
atgattgtgg tattttggaga tgaacctcca gtcttctctc gtccttatttc ggcattctat 540
ccgccataacc aggcaacggg gccaccaaacttccata tgccaggcat gccagggtgga 600
atctctccat acccatccgg ataccctccc aatcccagt gttaccagg ctgtccttac 660
ccacctggtg gtccatatcc tgccacaaca agttctcagt acccttctca gcctcctgtg 720
accactgttg gtcccagtag ggtatggcaca atcagcgagg acaccatccg agcctctctc 780
atctctgcgg tcagtgacaa actgagatgg cggatgaagg aggaaatgga tcgtgcccag 840
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gaagagatgg ttacccgtt agatcaagaa gtagccgagg ttgataaaaa catagaacct	960
ttgaaaaaga aggatgaaga actcagttct gctctggaaa aaatggaaaa tcagtctgaa	1020
aacaatgata tcgatgaagt tatcattccc acagctccct tatacaaaca gatcctgaat	1080
ctgtatgcag aagaaaacgc tattgaagac actatcttt acttggaga agccttgaga	1140
aggggcgtga tagacctgga tgtcttcctg aagcatgtac gtctctgtc ccgtaaacag	1200
ttccagctga gggcactaat gcaaaaagca agaaagactg ccggtctcag tgacctctac	1260
tgacttctct gataccagct ggaggtttag ctcttcttaa agtattcttc tcttccttt	1320
atcagtaggt gcccagaata agttattgca gtttatcatt caagtgtaaa atatttgaa	1380
tcaataatat attttctgtt ttcttttgtt aaagactggc ttttattaat gcactttcta	1440
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Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
20 25 30

Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
 35 40 45

Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
50 55 60

Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
 65 70 75 80

Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
 85 80 85

Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
100 105 110

Tyr-Leu-His-Glu-Trp-Lys-His-Pro-Gln-Ser-Asp-Leu-Leu-Gly-Leu-Ile

115

120

125

Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
130 135 140

Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
145 150 155 160

Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
165 170 175

Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
180 185 190

Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro
195 200 205

Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
210 215 220

Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
225 230 235 240

Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu
245 250 255

Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu
260 265 270

Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile
275 280 285

Glu Leu Leu Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys
290 295 300

Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro
305 310 315 320

Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn
325 330 335

Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly
340 345 350

Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser Arg

355

360

365

Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala
370 375 380

Gly Leu Ser Asp Leu Tyr
385 390

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<220>
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27

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<213> Artificial Sequence

<220>
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<400> 6
caucuccaaa uaccacaauc augaccu

27

<210> 7
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<212> RNA
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39

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39

<210> 9

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<211> 28
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<210> 10
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<212> DNA
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<400> 10
attttagcagt cccaacattc agcacaaaa                                28

<210> 11
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<212> DNA
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<220>
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gagaccgacc tctccgtaaa gcattctt                                28

<210> 12
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<220>
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<400> 12
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<210> 13
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attttagcagt cccaacattc agcacaaaa                                28

<210> 14

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<211> 25		
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<211> 9
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<220>
<223> Primer

<400> 19

His Thr His Leu Ala Met Asx Asp Ala
1 5

<210> 20
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<220>
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<220>
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<222> (2)..(2)
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<400> 20

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1 5 10